

PCT09

RAW SEQUENCE LISTING

DATE: 12/21/2001

PATENT APPLICATION: US/09/980,881

TIME: 13:01:21

Input Set : A:\MAT-101PCTsq.txt

Output Set: N:\CRF3\12212001\I980881.raw

ENTERED

3 <110> APPLICANT: AKIRA MATSUMOTO
 5 <120> TITLE OF INVENTION: Human Brain Carboxypeptidase B
 7 <130> FILE REFERENCE: MAT-101PCT
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/980,881
 C--> 10 <141> CURRENT FILING DATE: 2001-10-30
 12 <150> PRIOR APPLICATION NUMBER: JP 1999-125169
 13 <151> PRIOR FILING DATE: 1999-04-30
 15 <160> NUMBER OF SEQ ID NOS: 9
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1573
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (18)..(1097)
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 30 Met Lys Leu Cys Ser Leu Ala Val Leu Val Pro
 31 1 5 10
 33 att gtt ctc ttc tgt gag cag cat gtc ttc gcg ttc cag agt ggc caa 98
 34 Ile Val Leu Phe Cys Glu Gln His Val Phe Ala Phe Gln Ser Gly Gln
 35 15 20 25
 37 gtt cta gct gct ctt cct aga acc tct agg caa gtt caa gtt cta cag 146
 38 Val Leu Ala Ala Leu Pro Arg Thr Ser Arg Gln Val Gln Val Leu Gln
 39 30 35 40
 41 aat ctt act aca aca tat gag att gtt ctc tgg cag ccg gta aca gct 194
 42 Asn Leu Thr Thr Thr Tyr Glu Ile Val Leu Trp Gln Pro Val Thr Ala
 43 45 50 55
 45 gac ctt att gtg aag aaa aaa caa gtc cat ttt ttt gta aat gca tct 242
 46 Asp Leu Ile Val Lys Lys Lys Gln Val His Phe Phe Val Asn Ala Ser
 47 60 65 70 75
 49 gat gtc gac aat gtg aaa gcc cat tta aat gtg agc gga att cca tgc 290
 50 Asp Val Asp Asn Val Lys Ala His Leu Asn Val Ser Gly Ile Pro Cys
 51 80 85 90
 53 agt gtc ttg ctg gca gac gtg gaa gat ctt att caa cag cag att tcc 338
 54 Ser Val Leu Leu Ala Asp Val Glu Asp Leu Ile Gln Gln Gln Ile Ser
 55 95 100 105
 57 aac gac aca gtc agc ccc cga gcc tcc gca tcg tac tat gaa cag tat 386
 58 Asn Asp Thr Val Ser Pro Arg Ala Ser Ala Ser Tyr Tyr Glu Gln Tyr
 59 110 115 120
 61 cac tca cta aat gaa atc tat tct tgg ata gaa ttt ata act gag agg 434
 62 His Ser Leu Asn Glu Ile Tyr Ser Trp Ile Glu Phe Ile Thr Glu Arg
 63 125 130 135
 65 cat cct gat atg ctt aca aaa atc cac att gga tcc tca ttt gag aag 482
 66 His Pro Asp Met Leu Thr Lys Ile His Ile Gly Ser Ser Phe Glu Lys
 67 140 145 150 155

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69 tac cca ctc tat gtt tta aag gtt tct gga aaa gaa caa aca gcc aaa 530
70 Tyr Pro Leu Tyr Val Leu Lys Val Ser Gly Lys Glu Gln Thr Ala Lys
71 160 165 170
73 aat gcc ata tgg att gac tgt gga atc cat gcc aga gaa tgg atc tct 578
74 Asn Ala Ile Trp Ile Asp Cys Gly Ile His Ala Arg Glu Trp Ile Ser
75 175 180 185
77 cct gct ttc tgc ttg tgg ttc ata ggc cat aat cga atg tgg aga aag 626
78 Pro Ala Phe Cys Leu Trp Phe Ile Gly His Asn Arg Met Trp Arg Lys
79 190 195 200
81 aac cgt tct ttc tat gcg aac aat cat tgc atc gga aca gac ctg aat 674
82 Asn Arg Ser Phe Tyr Ala Asn Asn His Cys Ile Gly Thr Asp Leu Asn
83 205 210 215
85 agc aac ttt gtc tcc aaa cac tgg tgt gag gaa ggt gca tcc agt tcc 722
86 Ser Asn Phe Val Ser Lys His Trp Cys Glu Glu Gly Ala Ser Ser Ser
87 220 225 230 235
89 tca tgc tcg gaa acc tac tgt gga ctt tat cct gag tca gaa cca gaa 770
90 Ser Cys Ser Glu Thr Tyr Cys Gly Leu Tyr Pro Glu Ser Glu Pro Glu
91 240 245 250
93 gtg aag gca gtg gct agt ttc ttg aga aga aat atc aac cag att aaa 818
94 Val Lys Ala Val Ala Ser Phe Leu Arg Arg Asn Ile Asn Gln Ile Lys
95 255 260 265
97 gca tac atc agc atg cat tca tac tcc cag cat ata gtg ttt cca tat 866
98 Ala Tyr Ile Ser Met His Ser Tyr Ser Gln His Ile Val Phe Pro Tyr
99 270 275 280
101 tcc tat aca cga agt aaa agc aaa gac cat gag gaa ctg tct cta gta 914
102 Ser Tyr Thr Arg Ser Lys Ser Lys Asp His Glu Glu Leu Ser Leu Val
103 285 290 295
105 gcc agt gaa gca gtt cgt gct att gac aaa act agt aaa aat acc agg 962
106 Ala Ser Glu Ala Val Arg Ala Ile Asp Lys Thr Ser Lys Asn Thr Arg
107 300 305 310 315
109 tat aca cat ggc cat ggc tca gaa acc tta tac cta gct cct gga ggt 1010
110 Tyr Thr His Gly His Gly Ser Glu Thr Leu Tyr Leu Ala Pro Gly Gly
111 320 325 330
113 ggg gac gat tgg atc tat gat ttg ggc atc aaa tat tcg ttt aca tca 1058
114 Gly Asp Asp Trp Ile Tyr Asp Leu Gly Ile Lys Tyr Ser Phe Thr Ser
115 335 340 345
117 aac cca cct gta gag aag ctt ttg ccg ctg tct cta aaa tagcttgga 1107
118 Asn Pro Pro Val Glu Lys Leu Leu Pro Leu Ser Leu Lys
119 350 355 360
121 tgtcattagg aatgtttaat gcccttgatt ttatcattct gcttcggtat ttttaatttac 1167
123 tgattccagc aagaccaaatt cattgtatca gattatTTTT aagttttatc cgtagtTTTT 1227
125 ataaaagatt ttctatttcc ttggttctgt cagagaacct aataagtgtc acttttgccat 1287
127 taaggcagac tagggttcat gtctttttac cctttaaaaa aaaattgtaa aagtctagtt 1347
129 acctactttt tctttgattt tcgacgtttg actagccatc tcaagcaact ttcgacgttt 1407
131 gactagccat ctcaagcaag tttaatcaaa gatcatotca cgctgatcat tggatcctac 1467
133 tcaacaaaag gaagggtggt cagaagtaca ttaaagattt ctgctccaaa ttttcaataa 1527
135 attttcttctt ctcttttaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1573
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 360

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140 <212> TYPE: PRT
 141 <213> ORGANISM: Homo sapiens
 143 <400> SEQUENCE: 2 Δ^3
 144 Met Lys Leu Cys Ser Leu Ala Val Leu Val Pro Ile Val Leu Phe Cys
 145 1 5 10 15
 147 Glu Gln His Val Phe Ala Phe Gln Ser Gly Gln Val Leu Ala Ala Leu
 148 20 25 30
 150 Pro Arg Thr Ser Arg Gln Val Gln Val Leu Gln Asn Leu Thr Thr Thr
 151 35 40 45
 153 Tyr Glu Ile Val Leu Trp Gln Pro Val Thr Ala Asp Leu Ile Val Lys
 154 50 55 60
 156 Lys Lys Gln Val His Phe Phe Val Asn Ala Ser Asp Val Asp Asn Val
 157 65 70 75 80
 159 Lys Ala His Leu Asn Val Ser Gly Ile Pro Cys Ser Val Leu Leu Ala
 160 85 90 95
 162 Asp Val Glu Asp Leu Ile Gln Gln Gln Ile Ser Asn Asp Thr Val Ser
 163 100 105 110
 165 Pro Arg Ala Ser Ala Ser Tyr Tyr Glu Gln Tyr His Ser Leu Asn Glu
 166 115 120 125
 168 Ile Tyr Ser Trp Ile Glu Phe Ile Thr Glu Arg His Pro Asp Met Leu
 169 130 135 140
 171 Thr Lys Ile His Ile Gly Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val
 172 145 150 155 160
 174 Leu Lys Val Ser Gly Lys Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile
 175 165 170 175
 177 Asp Cys Gly Ile His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu
 178 180 185 190
 180 Trp Phe Ile Gly His Asn Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr
 181 195 200 205
 183 Ala Asn Asn His Cys Ile Gly Thr Asp Leu Asn Ser Asn Phe Val Ser
 184 210 215 220
 186 Lys His Trp Cys Glu Glu Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr
 187 225 230 235 240
 189 Tyr Cys Gly Leu Tyr Pro Glu Ser Glu Pro Glu Val Lys Ala Val Ala
 190 245 250 255
 192 Ser Phe Leu Arg Arg Asn Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met
 193 260 265 270
 195 His Ser Tyr Ser Gln His Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser
 196 275 280 285
 198 Lys Ser Lys Asp His Glu Glu Leu Ser Leu Val Ala Ser Glu Ala Val
 199 290 295 Same as 300
 201 Arg Ala Ile Asp Lys Thr Ser Lys Asn Thr Arg Tyr Thr His Gly His
 202 305 310 315 320
 204 Gly Ser Glu Thr Leu Tyr Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile
 205 325 330 335
 207 Tyr Asp Leu Gly Ile Lys Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu
 208 340 345 350
 210 Lys Leu Leu Pro Leu Ser Leu Lys
 211 355 360

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Input Set : A:\MAT-101PCTsq.txt

Output Set: N:\CRF3\12212001\I980881.raw

214 <210> SEQ ID NO: 3
 215 <211> LENGTH: 338
 216 <212> TYPE: PRT
 217 <213> ORGANISM: Homo sapiens
 219 <400> SEQUENCE: 3
 220 Phe Gln Ser Gly Gln Val Leu Ala Ala Leu Pro Arg Thr Ser Arg Gln
 221 1 5 10 15
 223 Val Gln Val Leu Gln Asn Leu Thr Thr Thr Tyr Glu Ile Val Leu Trp
 224 20 25 30
 226 Gln Pro Val Thr Ala Asp Leu Ile Val Lys Lys Lys Gln Val His Phe
 227 35 40 45
 229 Phe Val Asn Ala Ser Asp Val Asp Asn Val Lys Ala His Leu Asn Val
 230 50 55 60
 232 Ser Gly Ile Pro Cys Ser Val Leu Leu Ala Asp Val Glu Asp Leu Ile
 233 65 70 75 80
 235 Gln Gln Gln Ile Ser Asn Asp Thr Val Ser Pro Arg Ala Ser Ala Ser
 236 85 90 95
 238 Tyr Tyr Glu Gln Tyr His Ser Leu Asn Glu Ile Tyr Ser Trp Ile Glu
 239 100 105 110
 241 Phe Ile Thr Glu Arg His Pro Asp Met Leu Thr Lys Ile His Ile Gly
 242 115 120 125
 244 Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val Leu Lys Val Ser Gly Lys
 245 130 135 140
 247 Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile Asp Cys Gly Ile His Ala
 248 145 150 155 160
 250 Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu Trp Phe Ile Gly His Asn
 251 165 170 175
 253 Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr Ala Asn Asn His Cys Ile
 254 180 185 190
 256 Gly Thr Asp Leu Asn Arg Asn Phe Ala Ser Lys His Trp Cys Glu Glu
 257 195 200 205
 259 Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr Tyr Cys Gly Leu Tyr Pro
 260 210 215 220
 262 Glu Ser Glu Pro Glu Val Lys Ala Val Ala Ser Phe Leu Arg Arg Asn
 263 225 230 235 240
 265 Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met His Ser Tyr Ser Gln His
 266 245 250 255
 268 Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser Lys Ser Lys Asp His Glu
 269 260 265 270
 271 Glu Leu Ser Leu Val Ala Ser Glu Ala Val Arg Ala Ile Glu Lys Thr
 272 275 280 285
 274 Ser Lys Asn Thr Arg Tyr Thr His Gly His Gly Ser Glu Thr Leu Tyr
 275 290 295 300
 277 Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile Tyr Asp Leu Gly Ile Lys
 278 305 310 315 320
 280 Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu Lys Leu Leu Pro Leu Ser
 281 325 330 335
 283 Leu Lys
 287 <210> SEQ ID NO: 4

20020201 09080881

366
 -336
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Input Set : A:\MAT-101PCTsq.txt

Output Set: N:\CRF3\12212001\I980881.raw

288 <211> LENGTH: 246
 289 <212> TYPE: PRT
 290 <213> ORGANISM: Homo sapiens
 292 <400> SEQUENCE: 4
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 296 Ser Trp Ile Glu Phe Ile Thr Glu Arg His Pro Asp Met Leu Thr Lys
 297 20 25 30
 299 Ile His Ile Gly Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val Leu Lys
 300 35 40 45
 302 Val Ser Gly Lys Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile Asp Cys
 303 50 55 60
 305 Gly Ile His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu Trp Phe
 306 65 70 75 80
 308 Ile Gly His Asn Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr Ala Asn
 309 85 90 95
 311 Asn His Cys Ile Gly Thr Asp Leu Asn Arg Asn Phe Ala Ser Lys His
 312 100 105 110
 314 Trp Cys Glu Glu Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr Tyr Cys
 315 115 120 125
 317 Gly Leu Tyr Pro Glu Ser Glu Pro Glu Val Lys Ala Val Ala Ser Phe
 318 130 135 140
 320 Leu Arg Arg Asn Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met His Ser
 321 145 150 155 160
 323 Tyr Ser Gln His Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser Lys Ser
 324 165 170 175
 326 Lys Asp His Glu Glu Leu Ser Leu Val Ala Ser Glu Ala Val Arg Ala
 327 180 185 190
 329 Ile Glu Lys Thr Ser Lys Asn Thr Arg Tyr Thr His Gly His Gly Ser
 330 195 200 205
 332 Glu Thr Leu Tyr Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile Tyr Asp
 333 210 215 220
 335 Leu Gly Ile Lys Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu Lys Leu
 336 225 230 235 240
 338 Leu Pro Leu Ser Leu Lys
 339 245
 342 <210> SEQ ID NO: 5
 343 <211> LENGTH: 24
 344 <212> TYPE: PRT
 345 <213> ORGANISM: Artificial Sequence
 347 <220> FEATURE:
 348 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificially
 349 synthesized oligopeptide sequence
 351 <400> SEQUENCE: 5
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 353 1 5 10 15
 355 Asn Pro Thr Tyr Lys Phe Phe Glu
 356 20
 359 <210> SEQ ID NO: 6

VERIFICATION SUMMARY

DATE: 12/21/2001

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TIME: 13:01:23

Input Set : A:\MAT-101PCTsq.txt

Output Set: N:\CRF3\12212001\I980881.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

20021221 13:01:23 I980881.032802